- (a) generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:
 - (i) a first value for a first polynucleotide characteristic.
- (ii) a second value for a second polynucleotide-characteristic different from said first characteristic, and
 - (iii) a third value that is a measure of the quantity of the polynucleotide;
- (b) calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and
- (c) displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression, and further comprising:
- (d) generating a file containing information for display relating to a peak in the molecular topology, and
- (e) linking the information for display to the related peak in the molecular topography.
- 3. (Amended) A method in a computer system for analyzing an displaying data on gene expression in a molecular topography, comprising:
- (a) generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:
 - (i) a first value for a first polynucleotide characteristic.

- (ii) a second value for a second polynucleotide-characteristic different from said first characteristic, and
 - (iii) a third value that is a measure of the quantity of the polynucleotide:
- (b) calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and
- (c) displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression,

wherein: (i) the first characteristic is a sequence identifier, and (ii) the second characteristic is a measure of size.

- 5. (Amended) The method of Claim 2, wherein the polynucleotides are cDNAs or fragments thereof.
- 6. (Amended) A method in a computer system for analyzing an displaying data on gene expression in a molecular topography, comprising:
- (a) generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:
 - (i) a first value for a first polynucleotide characteristic.
- (ii) a second value for a second polynucleotide-characteristic different from said first characteristic, and
 - (iii) a third value that is a measure of the quantity of the polynucleotide;

- (b) calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and
- (c) displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression,

wherein the polynucleotides are cDNAs or fragments thereof, and wherein the polynucleotides are 3'-end fragments of restriction enzyme cleaved cDNAs.

- 11. (Amended) A method in a computer system for displaying differences in gene expression, comprising:
- (1) for each of two gene expression profiles to be compared generating a molecular topography according to a method in a computer system for analyzing an displaying data on gene expression in a molecular topography, comprising:
- (a) generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:
 - (i) a first value for a first polynucleotide characteristic,
- (ii) a second value for a second polynucleotide-characteristic different from said first characteristic, and
 - (iii) a third value that is a measure of the quantity of the polynucleotide;
- (b) calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

- (c) displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression.
- (2) for each position in the two co-ordinate space subtracting the measure of quantity in the first profile from the measure of quantity in the second profile;
 - (3) for each position, generating a peak for display from the difference; and
- (4) displaying the respective difference peak at each of the positions in the two coordinate space.
- 12. (Amended) A method in a computer system for displaying differences in gene expression, comprising:
- (1) for each of two gene expression profiles to be compared generating a molecular topography according to a method, comprising:
- (a) generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:
 - (i) a first value for a first polynucleotide characteristic,
- (ii) a second value for a second polynucleotide-characteristic different from said first characteristic, and
 - (iii) a third value that is a measure of the quantity of the polynucleotide;
- (b) calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

- (c) displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression.
- (2) for each position in the two co-ordinate space subtracting the measure of quantity in the first profile from the measure of quantity in the second profile;
 - (3) for each position, generating a peak for display from the difference; and
- (4) displaying the respective difference peak at each of the positions in the two coordinate space,

wherein differences are displayed only if they meet or exceed a threshold value.

- 23. (Twice amended) A method in a computer system for displaying a series of in gene expression profiles in a molecular movie, comprising:
- (1) generating a plurality of molecular topographies according to a method, comprising:
- (a) generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:
 - (i) a first value for a first polynucleotide characteristic,
- (ii) a second value for a second polynucleotide-characteristic different from said first characteristic, and
 - (iii) a third value that is a measure of the quantity of the polynucleotide;
- (b) calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

- (c) displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression, and
 - (2) displaying the molecular topographies in succession, wherein the molecular topographies are delta plots.
- 24. (Amended) A computer program product, usable in a computer system, for analyzing and displaying gene expression in a molecular topography, the computer program product comprising:

a first program code that generates a gene expression profile of a plurality of geneexpression indicating polynucleotides including for each of the polynucleotides:

- (i) a first value for a first polynucleotide characteristic,
- (ii) a second value for a second polynucleotide- characteristic different from said first characteristic, and
- (iii) a third value that is a measure of the quantity of the polynucleotide; a second program code that calculates for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

a third program code that displays the peak for each polynucleotide at the calculated position for the polynucleotide in a display, the resulting display resulting thereby a molecular topography of gene expression, and further comprising

(d) a fourth program code for generating a file containing information for display relating to a peak in the molecular topology, and